25

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> Novel cytochrome P450 monooxygenases and their use for the oxidation of organic substrates

<130> M/40241

<140>
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<160> 9

<170> PatentIn Ver. 2.1

<210> 1
<211> 3150
<212> DNA
<213> Bacillus megaterium

<220>
<221> CDS
<222> (4)..(3150)

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    1               5                   10                  15

aat tta ccg tta tta aac aca gat aaa ccg gtt caa gct ttg atg aaa      96
Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys
                20                  25                  30

att gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt     144
Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg
                35                  40                  45

gta acg cgc tac tta tca agt cag cgt cta att aaa gaa gca tgc gat     192
Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp
            50                  55                  60

gaa tca cgc ttt gat aaa aac tta agt caa gcg ctt aaa ttt gta cgt     240
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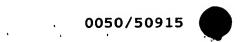
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gat ttt gca gga gac ggg tta ttt aca agc tgg acg cat gaa aaa aat    288
Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn
 80              85                  90                  95

tgg aaa aaa gcg cat aat atc tta ctt cca agc ttc agt cag cag gca    336
Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala
                100                 105                 110

atg aaa ggc tat cat gcg atg atg gtc gat atc gcc gtg cag ctt gtt    384
Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val
                115                 120                 125

caa aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa    432
Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu
                130                 135                 140

gac atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac    480
Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn
        145                 150                 155

tat cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca    528
Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr
160             165                 170                 175

agt atg gtc cgt gca ctg gat gaa gca atg aac aag ctg cag cga gca    576
Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala
                180                 185                 190

aat cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa    624
Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu
                195                 200                 205

gat atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc    672
Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg
                210                 215                 220

aaa gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac    720
Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn
        225                 230                 235

gga aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc    768
Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg
240             245                 250                 255

tat caa att att aca ttc tta att gcg gga cac gaa aca aca agt ggt    816
Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly
                260                 265                 270

ctt tta tca ttt gcg ctg tat ttc tta gtg aaa aat cca cat gta tta    864
Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu
                275                 280                 285
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caa aaa gca gca gaa gaa gca gca cga gtt cta gta gat cct gtt cca    912
Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro
        290             295             300

agc tac aaa caa gtc aaa cag ctt aaa tat gtc ggc atg gtc tta aac    960
Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn
        305             310             315

gaa gcg ctg cgc tta tgg cca act gct cct gcg ttt tcc cta tat gca   1008
Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala
320             325             330             335

aaa gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac   1056
Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp
                340             345             350

gaa cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg   1104
Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp
            355             360             365

gga gac gat gtg gaa gag ttc cgt cca gag cgt ttt gaa aat cca agt   1152
Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser
            370             375             380

gcg att ccg cag cat gcg ttt aaa ccg ttt gga aac ggt cag cgt gcg   1200
Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala
        385             390             395

tgt atc ggt cag cag ttc gct ctt cat gaa gca acg ctg gta ctt ggt   1248
Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly
400             405             410             415

atg atg cta aaa cac ttt gac ttt gaa gat cat aca aac tac gag ctg   1296
Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu
            420             425             430

gat att aaa gaa act tta acg tta aaa cct gaa ggc ttt gtg gta aaa   1344
Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys
            435             440             445

gca aaa tcg aaa aaa att ccg ctt ggc ggt att cct tca cct agc act   1392
Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr
        450             455             460

gaa cag tct gct aaa aaa gta cgc aaa aag gca gaa aac gct cat aat   1440
Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn
        465             470             475

acg ccg ctg ctt gtg cta tac ggt tca aat atg gga aca gct gaa gga   1488
Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly
480             485             490             495
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28

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acg gcg cgt gat tta gca gat att gca atg agc aaa gga ttt gca ccg    1536
Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro
            500                 505                 510


cag gtc gca acg ctt gat tca cac gcc gga aat ctt ccg cgc gaa gga    1584
Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly
            515                 520                 525


gct gta tta att gta acg gcg tct tat aac ggt cat ccg cct gat aac    1632
Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn
            530                 535                 540


gca aag caa ttt gtc gac tgg tta gac caa gcg tct gct gat gaa gta    1680
Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val
            545                 550                 555


aaa ggc gtt cgc tac tcc gta ttt gga tgc ggc gat aaa aac tgg gct    1728
Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala
560                 565                 570                 575


act acg tat caa aaa gtg cct gct ttt atc gat gaa acg ctt gcc gct    1776
Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala
            580                 585                 590


aaa ggg gca gaa aac atc gct gac cgc ggt gaa gca gat gca agc gac    1824
Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp
            595                 600                 605


gac ttt gaa ggc aca tat gaa gaa tgg cgt gaa cat atg tgg agt gac    1872
Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp
            610                 615                 620


gta gca gcc tac ttt aac ctc gac att gaa aac agt gaa gat aat aaa    1920
Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys
            625                 630                 635


tct act ctt tca ctt caa ttt gtc gac agc gcc gcg gat atg ccg ctt    1968
Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu
640                 645                 650                 655


gcg aaa atg cac ggt gcg ttt tca acg aac gtc gta gca agc aaa gaa    2016
Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu
                    660                 665                 670


ctt caa cag cca ggc agt gca cga agc acg cga cat ctt gaa att gaa    2064
Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu
                    675                 680                 685


ctt cca aaa gaa gct tct tat caa gaa gga gat cat tta ggt gtt att    2112
Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile
            690                 695                 700
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cct cgc aac tat gaa gga ata gta aac cgt gta aca gca agg ttc ggc     2160
Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly
    705                 710                 715

cta gat gca tca cag caa atc cgt ctg gaa gca gaa gaa gaa aaa tta     2208
Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu
720                 725                 730                 735

gct cat ttg cca ctc gct aaa aca gta tcc gta gaa gag ctt ctg caa     2256
Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln
                740                 745                 750

tac gtg gag ctt caa gat cct gtt acg cgc acg cag ctt cgc gca atg     2304
Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met
                755                 760                 765

gct gct aaa acg gtc tgc ccg ccg cat aaa gta gag ctt gaa gcc ttg     2352
Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu
                770                 775                 780

ctt gaa aag caa gcc tac aaa gaa caa gtg ctg gca aaa cgt tta aca     2400
Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr
        785                 790                 795

atg ctt gaa ctg ctt gaa aaa tac ccg gcg tgt gaa atg aaa ttc agc     2448
Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser
800                 805                 810                 815

gaa ttt atc gcc ctt ctg cca agc ata cgc ccg cgc tat tac tcg att     2496
Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile
                820                 825                 830

tct tca tca cct cgt gtc gat gaa aaa caa gca agc atc acg gtc agc     2544
Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser
                835                 840                 845

gtt gtc tca gga gaa gcg tgg agc gga tat gga gaa tat aaa gga att     2592
Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile
        850                 855                 860

gcg tcg aac tat ctt gcc gag ctg caa gaa gga gat acg att acg tgc     2640
Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys
        865                 870                 875

ttt att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa     2688
Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu
880                 885                 890                 895

acg ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga     2736
Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg
                900                 905                 910
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30

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ggc ttt gtg cag gcg cgc aaa cag cta aaa gaa caa gga cag tca ctt    2784
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            915                 920                 925


gga gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat    2832
Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr
            930                 935                 940


ctg tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg    2880
Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr
            945                 950                 955


ctt cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt    2928
Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val
960                 965                 970                 975


cag cac gta atg gaa caa gac ggc aag aaa ttg att gaa ctt ctt gat    2976
Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp
                    980                 985                 990


caa gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct    3024
Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro
                995                 1000                1005


gcc gtt gaa gca acg ctt atg aaa agc tat gct gac gtt cac caa gtg    3072
Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
            1010                1015                1020


agt gaa gca gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa ggc    3120
Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly
            1025                1030                1035


cga tac gca aaa gac gtg tgg gct ggg taa                            3150
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<211> 1048
<212> PRT
<213> Bacillus megaterium

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            20              25                  30


Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val
        35              40                  45
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31

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Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu
    50              55              60

Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp
    65          70              75              80

Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn Trp
            85              90              95

Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
            100             105             110

Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
        115             120             125

Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp
    130             135             140

Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr
145             150             155             160

Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser
            165             170             175

Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn
            180             185             190

Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp
            195             200             205

Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys
    210             215             220

Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly
225             230             235             240

Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr
            245             250             255

Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu
            260             265             270

Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln
            275             280             285

Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser
    290             295             300

Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu
305             310             315             320
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32

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Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys
            325             330             335

Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu
            340             345             350

Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly
            355             360             365

Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala
    370             375             380

Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys
385             390             395             400

Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met
            405             410             415

Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp
            420             425             430

Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala
            435             440             445

Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu
    450             455             460

Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr
465             470             475             480

Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr
            485             490             495

Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln
            500             505             510

Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala
            515             520             525

Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala
    530             535             540

Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys
545             550             555             560

Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr
            565             570             575

Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys
            580             585             590
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33

Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp Asp
        595   600   605

Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val
    610   615   620

Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys Ser
625   630   635   640

Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu Ala
                645   650   655

Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu
            660   665   670

Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu
        675   680   685

Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro
    690   695   700

Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly Leu
705   710   715   720

Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu Ala
            725   730   735

His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr
            740   745   750

Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala
        755   760   765

Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu
    770   775   780

Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met
785   790   795   800

Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser Glu
            805   810   815

Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile Ser
        820   825   830

Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val
        835   840   845

Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala
850   855   860

Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe
865   870   875   880

Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr
            885   890   895

Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly
            900   905   910

Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly
            915   920   925

Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu
        930   935   940

Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu
945   950   955   960

His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln
            965   970   975

His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln
            980   985   990

Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala
        995   1000   1005

Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val Ser
    1010   1015   1020

Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly Arg
1025   1030   1035   1040

Tyr Ala Lys Asp Val Trp Ala Gly
            1045

<210> 3
<211> 30
<212> DNA
<213> Synthetic sequence

<220>
<223> Description of the synthetic sequence: PCR primer

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gcaggagacg ggttgnnnac aagctggacg   30

<210> 4
<211> 30
<212> DNA
<213> Synthetic sequence

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<220>
<223> Description of the synthetic sequence: PCR primer


<400> 4
cgtccagctt gtnnncaacc cgtctcctgc                                    30


<210> 5
<211> 34
<212> DNA
<213> Synthetic sequence


<220>
<223> Description of the synthetic sequence: PCR primer


<400> 5
gaagcaatga acaagnnnca gcgagcaaat ccag                               34


<210> 6
<211> 30
<212> DNA
<213> Synthetic sequence


<220>
<223> Description of the synthetic sequence: PCR primer


<400> 6
ctggatttgc tcgctgnnnc ttgttcattg                                    30


<210> 7
<211> 41
<212> DNA
<213> Synthetic sequence


<220>
<223> Description of the synthetic sequence: PCR primer


<400> 7
gctttgataa aaacttaaag tcaannnctt aaatttgtac g                       41


<210> 8
<211> 40
<212> DNA
<213> Synthetic sequence


<220>
<223> Description of the synthetic sequence: PCR primer


<400> 8
cgtacaaatt taagnnnttg acttaagttt ttatcaaagc                         40
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<210> 9
<211> 1049
<212> PRT
<213> Bacillus megaterium

<400> 9
Met Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys
 1               5                  10                  15

Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys
                20                  25                  30

Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg
            35                  40                  45

Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp
        50                  55                  60

Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg
65                  70                  75                  80

Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn
                85                  90                  95

Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala
            100                 105                 110

Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val
        115                 120                 125

Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu
    130                 135                 140

Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn
145                 150                 155                 160

Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr
                165                 170                 175

Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala
            180                 185                 190

Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu
        195                 200                 205

Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg
    210                 215                 220

Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn
225                 230                 235                 240
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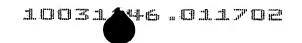
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Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg
                245             250             255

Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly
                260             265             270

Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu
                275             280             285

Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro
        290             295             300

Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn
305             310             315             320

Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala
                325             330             335

Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp
                340             345             350

Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp
                355             360             365

Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser
        370             375             380

Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala
385             390             395             400

Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly
                405             410             415

Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu
                420             425             430

Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys
                435             440             445

Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr
        450             455             460

Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn
465             470             475             480

Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly
                485             490             495

Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro
        500             505             510
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Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly
        515             520                 525

Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn
    530             535                 540

Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val
545             550                 555                 560

Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala
                565             570                 575

Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala
            580             585                 590

Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp
            595             600                 605

Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp
    610             615                 620

Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys
625             630                 635                 640

Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu
            645             650                 655

Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu
            660             665                 670

Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu
        675             680                 685

Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile
    690             695                 700

Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly
705             710                 715                 720

Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu
            725             730                 735

Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln
            740             745                 750

Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met
        755             760                 765

Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu
    770             775                 780
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Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr
785   790   795   800

Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser
            805   810   815

Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile
            820   825   830

Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser
            835   840   845

Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile
    850   855   860

Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys
865   870   875   880

Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu
            885   890   895

Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg
            900   905   910

Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu
            915   920   925

Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr
    930   935   940

Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr
945   950   955   960

Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val
            965   970   975

Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp
            980   985   990

Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro
            995   1000   1005

Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
    1010   1015   1020

Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly
1025   1030   1035   1040

Arg Tyr Ala Lys Asp Val Trp Ala Gly
            1045